



<110> Dayer, Jean-Michel  
Burger, Danielle  
Kohno, Tadahiko  
Edwards III, Carl K.

<120> APO-A-1 REGULATION OF T-CELL SIGNALING

<130> 06843.0035-00000

<140> 09/803,918  
<141> 2001-03-13

<150> 60/189,008  
<151> 2000-03-13

<150> 60/193,551  
<151> 2000-03-31

<160> 4

<170> PatentIn Ver. 2.1

<210> 1  
<211> 801  
<212> DNA  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> (1)..(72)

<400> 1  
atgaaagctg cgggtgctgac cttggccgtg ctcttcgtga cggggagcca ggctcgccat 60  
ttctggcagc aagatgaacc ccccccagac ccctgggatc gaggtaagga cctggccact 120  
gtgtacgtgg atgtgctcaa agacagcggc agagactatg tggccctggat tgaaggctcc 180  
gccttggaa aacagctaaa cctaaagctc cttgacaact gggacagcgt gacctccacc 240  
ttcagcaagc tgcgcgaaca gctcggccct gtgaccagg agttctggaa taacctggaa 300  
aaggagacag agggcctgag gcaggagatg agcaaggatc tggaggaggt gaaggccaag 360  
gtgcagccct accttggacga cttccagaag aagtggcagg aggagatgga gctctaccgc 420  
cagaaggtgg agccgcgtgc cgcagagctc caagagggcg cgccgcggaa gctgcacgag 480  
ctgcaagaga agctgagccc actgggcgag gagatgcgcg accgcgcgcg cgcccatgtg 540  
gacgcgcgtgc gcacgcacatc ggccccctac agcgacgcgc tgccgcgcg cttggccgcg 600  
cgccttgagg ctctcaagga gaacggcggc gccagactgg ccgagttacca cgccaaggcc 660  
accgagcatc tgagcacgct cagcgagaag gccaagccc cgctcgagga cctccgcca 720  
ggcctgctgc ccgtgctgga gagcttcaag gtcagcttcc tgagcgctct cgaggagttac 780  
actaagaagc tcaacaccca g 801

<210> 2  
<211> 267  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Lys Ala Ala Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser  
1 5 10 15  
Gln Ala Arg His Phe Trp Gln Gln Asp Glu Pro Pro Gln Ser Pro Trp  
20 25 30

## DAYER\_APP

Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp  
 35 40 45

Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys  
 50 55 60

Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr  
 65 70 75 80

Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp  
 85 90 95

Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys  
 100 105 110

Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe  
 115 120 125

Gln Lys Lys Trp Gln Glu Met Glu Leu Tyr Arg Gln Lys Val Glu  
 130 135 140

Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu  
 145 150 155 160

Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala  
 165 170 175

Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp  
 180 185 190

Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn  
 195 200 205

Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu  
 210 215 220

Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln  
 225 230 235 240

Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala  
 245 250 255

Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln  
 260 265

<210> 3  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(170)  
 <223> 18 kDa N-terminal fragment

<400> 3  
 Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr  
 1 5 10 15

Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln  
 20 25 30

## DAYER.APP

Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp  
 35 40 45

Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu  
 50 55 60

Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu  
 65 70 75 80

Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys  
 85 90 95

Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met  
 100 105 110

Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu  
 115 120 125

Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu  
 130 135 140

Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg  
 145 150 155 160

Thr His Leu Ala Pro Tyr Ser Asp Glu Leu  
 165 170

<210> 4  
 <211> 510  
 <212> DNA  
 <213> Homo sapiens

<400> 4  
 gatgaacccc cccagagccc ctgggatcga gtgaaggacc tggccactgt gtacgtggat 60  
 gtgctaaag acagcggcag agactatgtg tcccagttt aaggtccgc cttggaaaaa 120  
 cagctaaacc taaagctcct tgacaactgg gacagcgtga cctccacctt cagcaagctg 180  
 cgcgaacagc tcggccctgt gaccaggag ttctggata acctggaaaaa ggagacagag 240  
 ggcctgaggc aggagatgag caaggatctg gaggaggtga agggcaagggt gcagccctac 300  
 ctggacgact tccagaagaa gtggcaggag gagatggagc tctaccgcca gaaggtggag 360  
 ccgctgcgcg cagagctcca agagggcgcg cgccagaagc tgcacgagct gcaagagaag 420  
 ctgagccac tgggcgagga gatgcgcgac cgcgccgcg cccatgtgga cgcgctgcgc 480  
 acgcattctgg cccccctacag cgacgagctg 510